STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 171744

TO: Vanessa L Ford **Location: REM-3B25&2C18** 3C18 **Art Unit: 1645** **Monday, November 21, 2005** **Case Serial Number: 09/596101**	**From: Paul Schulwitz** **Location: Biotech-Chem Library** **REM-1A65** **Phone: 571-272-2527** **Paul.schulwitz@uspto.gov**

Search Notes

Examiner Ford,

Please review the attached search results.
If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
REM-1A65
571-272-2527

STIC-Biotech/ChemLib 17/744

From: Chan, Christina
Sent: Wednesday, November 16, 2005 12:17 PM
To: Ford, Vanessa; STIC-Biotech/ChemLib
Subject: RE: In e: 09/596,101 Sequence search

CRF

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From: Ford, Vanessa
Sent: Wednesday, November 16, 2005 9:57 AM
To: Chan, Christina
Subject: In e: 09/596,101 Sequence search

Please search SEQ ID NO:1 and 3. Please include interference searches. Please rush.

Vanessa L. Ford
Biotechnology Patent Examiner
Office: REM 3B25
Mailbox: REM 3C18
Phone: 571.272.0857
Art unit:1645

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 17, 2005, 16:55:19 ; Search time 1.57179 Seconds
(without alignments)
795.793 Million cell updates/sec

Title: US-09-596-101C-1
Perfect score: 64
Sequence: 1 SGEIDIIETIGNR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	70.3	294	2	D70525	probable beta-1 -
2	45	70.3	499	2	JC6141	beta 1,3-glucanase
3	44	68.8	301	2	C87296	beta-glucanase [im
4	43	67.2	411	2	JC7869	cell wall-lytic be
5	43	67.2	1356	2	E87311	DNA-directed RNA p
6	43	67.2	1377	2	AG3345	DNA-directed RNA p
7	43	67.2	1378	2	AB2817	DNA-directed RNA p
8	43	67.2	1411	2	C97595	RNA polymerase bet
9	41	64.1	736	2	T06757	hypothetical prote
10	40	62.5	815	2	B56708	extracellular sign
11	40	62.5	1302	2	T43230	DNA-directed RNA p
12	40	62.5	1342	1	RNEBBT	DNA-directed RNA p
13	40	62.5	1342	1	RNECB	DNA-directed RNA p
14	40	62.5	1342	1	S32680	DNA-directed RNA p
15	40	62.5	1342	2	A84934	DNA-directed RNA p
16	40	62.5	1342	2	C86090	RNA polymerase, be
17	40	62.5	1342	2	AE0933	DNA-directed RNA p
18	40	62.5	1342	2	F91242	RNA polymerase bet
19	40	62.5	1342	2	AC0456	DNA-directed RNA p
20	40	62.5	1343	1	H64073	DNA-directed RNA p
21	40	62.5	1375	2	F82336	DNA-directed RNA p
22	40	62.5	1389	2	T30824	RNA polymerase bet
23	40	62.5	1392	2	D82007	DNA-directed RNA p
24	40	62.5	1394	2	A81236	DNA-directed RNA p
25	40	62.5	1655	2	S47446	nucleoporin Np188
26	39	60.9	286	2	S48201	licheninase (EC 3.
27	39	60.9	369	2	AH0451	maltose/maltodextr
28	39	60.9	642	2	B72428	laminarinase - The
29	39	60.9	665	2	S52072	DmCNGC protein - f
30	39	60.9	795	2	A97627	hypothetical prote
31	39	60.9	795	2	AC2850	GGDEF family prote
32	39	60.9	967	2	T48210	hypothetical prote
33	39	60.9	1324	2	T18265	endo-1,3(4)-beta-g
34	38	59.4	263	2	A72349	conserved hypothet
35	38	59.4	298	2	S75156	hypothetical prote
36	38	59.4	371	1	MMECMK	inner membrane pro
37	38	59.4	371	2	B91256	inner membrane pro
38	38	59.4	371	2	F86096	inner membrane pro
39	38	59.4	544	2	T45498	hypothetical prote
40	38	59.4	608	2	T28301	ORF MSV140 hypothe
41	38	59.4	1103	2	T06918	DNA-directed RNA p
42	38	59.4	1143	2	S73173	DNA-directed RNA p
43	37	57.8	309	1	EUSMAG	agarase (EC 3.2.1.
44	37	57.8	316	2	T46000	hypothetical prote
45	37	57.8	625	2	G97076	alkaline phosphata

ALIGNMENTS

RESULT 1
D70525
probable beta-1 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70525
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70525
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-294 <COL>
A;Cross-references: UNIPROT:O07242; GB:Z96800; GB:AL123456; NID:g3261800; PIDN:CAB09586
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0315

Query Match 70.3%; Score 45; DB 2; Length 294;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 SGEIDIIETIGN 12
              |||||:||  ||
Db        169 SGEIDLIEWYGN 180
```

RESULT 2
JC6141
beta 1,3-glucanase (EC 3.2.1.-) precursor - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC6141; PC6037
R;Bachman, E.S.; McClay, D.R.
Proc. Natl. Acad. Sci. U.S.A. 93, 6808-6813, 1996
A;Title: Molecular cloning of the first metazoan beta-1,3 glucanase from eggs of the se
A;Reference number: JC6141; MUID:96270625; PMID:8692900
A;Accession: JC6141
A;Molecule type: mRNA
A;Residues: 1-499 <BAC>
A;Cross-references: UNIPROT:Q26660; GB:U49711; NID:g1488256; PIDN:AAC47235.1; PID:g1488
A;Accession: PC6037
A;Molecule type: protein
A;Residues: 21-40;197-209;329-344 <BA2>
A;Experimental source: egg
C;Comment: This enzyme functions in several extracellular activities including autocata efense enzymes in plants.
C;Keywords: egg; glycosidase; hydrolase

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 17, 2005, 16:55:04 ; Search time 5.9597 Seconds
(without alignments)
843.648 Million cell updates/sec

Title: US-09-596-101C-1
Perfect score: 64
Sequence: 1 SGEIDIIETIGNR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	100.0	13	2	AAY24915	Aay24915 Eisenia f
2	64	100.0	384	2	AAY24914	Aay24914 Eisenia f
3	50	78.1	306	2	AAR97362	Aar97362 Oerskovia
4	45	70.3	294	4	AAB52463	Aab52463 Mycobacte
5	44	68.8	263	2	AAW29455	Aaw29455 Oerskovia
6	44	68.8	303	2	AAW29457	Aaw29457 Oerskovia
7	44	68.8	435	2	AAW29456	Aaw29456 Oerskovia
8	43	67.2	384	4	AAB99272	Aab99272 Bacillus
9	43	67.2	1356	8	ADS27771	Ads27771 Bacterial
10	43	67.2	1357	8	ADS22522	Ads22522 Bacterial
11	43	67.2	1378	8	ADS22780	Ads22780 Bacterial
12	41	64.1	1356	8	ADS30542	Ads30542 Bacterial
13	40	62.5	185	4	ABG04199	Abg04199 Novel hum
14	40	62.5	205	4	AAU45016	Aau45016 Propionib
15	40	62.5	205	6	ABM41535	Abm41535 Propionib
16	40	62.5	254	4	ABG04191	Abg04191 Novel hum
17	40	62.5	434	7	ADM25572	Adm25572 Hyperther
18	40	62.5	501	4	ABG04189	Abg04189 Novel hum
19	40	62.5	533	8	ADR39768	Adr39768 Human kin
20	40	62.5	575	5	ABP27730	Abp27730 Streptoco
21	40	62.5	575	5	ABP29826	Abp29826 Streptoco
22	40	62.5	652	6	ABU45317	Abu45317 Protein e
23	40	62.5	815	7	ADF45054	Adf45054 Human kin
24	40	62.5	815	8	ADN05817	Adn05817 Antipsori
25	40	62.5	815	8	ADN88851	Adn88851 Human mit
26	40	62.5	816	8	ADQ20078	Adq20078 Human sof
27	40	62.5	816	8	ADQ15148	Adq15148 Human can
28	40	62.5	827	6	ABU25227	Abu25227 Protein e
29	40	62.5	987	8	ADL05331	Adl05331 M. catarr
30	40	62.5	1078	6	ABU27628	Abu27628 Protein e
31	40	62.5	1080	4	ABG04194	Abg04194 Novel hum
32	40	62.5	1173	6	ABU21190	Abu21190 Protein e
33	40	62.5	1342	4	AAU34845	Aau34845 E. coli c
34	40	62.5	1342	6	ABU47164	Abu47164 Protein e
35	40	62.5	1342	6	ABU14805	Abu14805 Protein e
36	40	62.5	1342	6	ABU49890	Abu49890 Protein e
37	40	62.5	1342	6	ABU39467	Abu39467 Protein e
38	40	62.5	1342	6	ABU47992	Abu47992 Protein e
39	40	62.5	1342	8	ADS42855	Ads42855 Bacterial
40	40	62.5	1342	8	ADS45221	Ads45221 Bacterial
41	40	62.5	1343	4	AAU35444	Aau35444 Haemophil
42	40	62.5	1343	6	ABU30272	Abu30272 Protein e
43	40	62.5	1351	6	ABM70460	Abm70460 Photorhab
44	40	62.5	1360	7	ABO60676	Abo60676 Klebsiell
45	40	62.5	1362	6	ABU17069	Abu17069 Protein e

ALIGNMENTS

RESULT 1
AAY24915
ID AAY24915 standard; peptide; 13 AA.
XX
AC AAY24915;
XX
DT 17-OCT-2003 (revised)
DT 25-AUG-1999 (first entry)
XX
DE Eisenia foetida coelomic cytolytic factor 1 peptide.
XX
KW Eisenia foetida; coelomic cytolytic factor 1; CCF-1; cancer;
KW trypanosomal infection; bacterial infection; tumour therapy;
KW inflammation; immunology.
XX
OS Eisenia fetida.
XX
PN WO9931229-A2.
XX
PD 24-JUN-1999.
XX
PF 16-DEC-1998; 98WO-EP008169.
XX
PR 17-DEC-1997; 97EP-00203974.
XX
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI De Baetselier P;
XX
DR WPI; 1999-385905/32.
XX
PT Eisenia foetida polypeptides derived from coelomic cytolytic factor 1.
XX
PS Claim 1; Page 45; 49pp; English.
XX
CC The present sequence represents a Eisenia foetida coelomic cytolytic
CC factor 1 (CCF-1) peptide. The CCF-1 protein has antiparasitic,
CC antibacterial and antiinflammatory activity. Recombinant coelomic
CC cytolytic factor 1 (rCCF-1) is trypanolytic for the African trypanosome
CC Trypanosoma brucei in a dose-dependent manner. The trypanolytic activity
CC of rCCF-1 can be inhibited by anti-CCF-1 and anti-tumour necrosis factor
CC (TNF)/TIP monoclonal antibodies. Furthermore, N,N'-diacetylchitobiose
CC inhibits potently trypanolytic activity of rCCF-1. These data corroborate
CC the findings that CCF-1 shares a trypanolytic, lectin-like domain with
CC TNF-alpha. CCF-1 is useful to treat trypanosomal or bacterial infections
CC or cancer. The proteins and peptides are also useful in tumour therapy,
CC inflammation and other areas of immunology. The annelid peptide is
CC derived from a 42 kDa cytolytic protein named CCF-1 that binds

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 17, 2005, 16:55:19 ; Search time 59.0025 Seconds
(without alignments)
485.831 Million cell updates/sec

Title: US-09-596-101C-3
Perfect score: 2240
Sequence: 1 MRWTLVVLCLLFGEGFAFTD.....DDEGDNNAMQVDYIRVYKRN 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	357	15.9	321	2	US-08-712-072C-3	Sequence 3, Appli
2	351.5	15.7	262	1	US-08-392-828C-37	Sequence 37, Appl
3	351.5	15.7	262	3	US-09-330-945-37	Sequence 37, Appl
4	350	15.6	303	3	US-09-159-106-13	Sequence 13, Appl
5	350	15.6	435	3	US-09-159-106-11	Sequence 11, Appl
6	344.5	15.4	276	2	US-08-712-072C-4	Sequence 4, Appli
7	340.5	15.2	263	3	US-09-159-106-2	Sequence 2, Appli
8	307	13.7	306	2	US-08-824-707-2	Sequence 2, Appli
9	286.5	12.8	285	2	US-08-712-072C-5	Sequence 5, Appli
10	272.5	12.2	422	2	US-08-712-072C-2	Sequence 2, Appli
11	231	10.3	470	4	US-09-902-540-16052	Sequence 16052, A
12	228.5	10.2	229	4	US-09-902-540-15416	Sequence 15416, A
13	208	9.3	654	1	US-08-392-828C-2	Sequence 2, Appli
14	208	9.3	654	3	US-09-330-945-2	Sequence 2, Appli
15	181	8.1	134	4	US-09-270-767-33162	Sequence 33162, A
16	163.5	7.3	176	4	US-09-270-767-44425	Sequence 44425, A
17	129.5	5.8	292	2	US-08-737-526-4	Sequence 4, Appli
18	129.5	5.8	292	3	US-09-098-580-4	Sequence 4, Appli
19	112.5	5.0	738	1	US-07-985-458-3	Sequence 3, Appli
20	112.5	5.0	954	4	US-09-570-856B-31	Sequence 31, Appl
21	111.5	5.0	622	3	US-09-311-626B-4	Sequence 4, Appli
22	110	4.9	243	3	US-09-286-690-10	Sequence 10, Appl
23	108	4.8	720	4	US-09-538-092-815	Sequence 815, App
24	107.5	4.8	545	3	US-09-269-731-8	Sequence 8, Appli
25	107.5	4.8	545	4	US-09-988-200-8	Sequence 8, Appli
26	106	4.7	238	3	US-09-286-690-7	Sequence 7, Appli
27	101.5	4.5	743	4	US-09-248-796A-17353	Sequence 17353, A
28	101	4.5	465	4	US-09-658-772-2	Sequence 2, Appli
29	101	4.5	465	4	US-10-159-487-2	Sequence 2, Appli
30	100	4.5	237	1	US-08-103-998-4	Sequence 4, Appli
31	99.5	4.4	1231	4	US-08-714-741-41	Sequence 41, Appl
32	99	4.4	279	3	US-09-286-690-9	Sequence 9, Appli
33	99	4.4	539	4	US-09-719-402A-2	Sequence 2, Appli
34	98.5	4.4	239	1	US-08-103-998-2	Sequence 2, Appli
35	98.5	4.4	308	4	US-09-463-862A-1	Sequence 1, Appli
36	96.5	4.3	685	4	US-09-252-991A-32033	Sequence 32033, A
37	96	4.3	478	4	US-09-107-532A-4922	Sequence 4922, Ap
38	96	4.3	814	4	US-09-486-072-1	Sequence 1, Appli
39	95	4.2	1722	4	US-09-194-612A-1	Sequence 1, Appli
40	94.5	4.2	276	4	US-09-719-402A-6	Sequence 6, Appli
41	94.5	4.2	1278	4	US-09-604-957-3	Sequence 3, Appli
42	93.5	4.2	1052	3	US-09-360-237-1	Sequence 1, Appli
43	93.5	4.2	1052	4	US-09-891-711-6	Sequence 6, Appli
44	93	4.2	829	4	US-09-252-991A-27150	Sequence 27150, A
45	92.5	4.1	312	3	US-09-216-295-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-712-072C-3
; Sequence 3, Application US/08712072C
; Patent No. 5925541
; GENERAL INFORMATION:
; APPLICANT: Jack Goldstein, Alex Zhu and Lin Leng
; TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amster, Rothstein & Ebenstein
; STREET: 90 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,072C
; FILING DATE: 11-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Elizabeth A.
; REGISTRATION NUMBER: 39,911
; REFERENCE/DOCKET NUMBER: 63475/97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: e13b, Bacillus circulars
US-08-712-072C-3

Query Match 15.9%; Score 357; DB 2; Length 321;

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 17, 2005, 16:55:04 ; Search time 176.04 Seconds
(without alignments)
843.648 Million cell updates/sec

Title: US-09-596-101C-3
Perfect score: 2240
Sequence: 1 MRWTLVVLCLLFGEGFAFTD.....DDEGDNNAMQVDYIRVYKRN 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2240	100.0	384	2	AAY24914	Eisenia f
2	357	15.9	492	4	ABB62773	Abb62773 Drosophil
3	350	15.6	303	2	AAW29457	Aaw29457 Oerskovia
4	350	15.6	435	2	AAW29456	Aaw29456 Oerskovia
5	340.5	15.2	263	2	AAW29455	Aaw29455 Oerskovia
6	314	14.0	455	2	AAR89136	Aar89136 Bombyx mo
7	314	14.0	467	2	AAR89137	Aar89137 Bombyx mo
8	310	13.8	261	2	AAR11599	Aar11599 Beta-1,3-
9	306	13.7	384	4	AAB99272	Aab99272 Bacillus
10	296	13.2	306	2	AAR97362	Aar97362 Oerskovia
11	295	13.2	490	4	ABB61180	Abb61180 Drosophil
12	286.5	12.8	422	2	AAW56275	Aaw56275 Flavobact
13	249.5	11.1	410	4	ABB60451	Abb60451 Drosophil
14	249.5	11.1	410	4	ABB60444	Abb60444 Drosophil
15	209	9.3	673	2	AAR67915	Aar67915 (1-3)-bet
16	209	9.3	673	6	ABR57645	Abr57645 Alpha sub
17	208	9.3	233	2	AAR67918	Aar67918 (1-3)-bet
18	184.5	8.2	845	4	AAB98062	Aab98062 Clostridi
19	168.5	7.5	341	2	AAW92310	Aaw92310 Streptomy
20	138.5	6.2	294	4	AAB52463	Aab52463 Mycobacte
21	131.5	5.9	292	2	AAR88406	Aar88406 Trichoder
22	121.5	5.4	424	2	AAW77311	Aaw77311 Phaffia r
23	117	5.2	437	5	ADF91891	Adf91891 Agarase I
24	115	5.1	975	5	ABP66068	Abp66068 Bifidobac
25	113.5	5.1	847	6	ABU31210	Abu31210 Protein e
26	113.5	5.1	875	2	AAW34987	Aaw34987 Bankia go
27	112.5	5.0	738	2	AAR20192	Aar20192 ADH compl
28	112.5	5.0	954	3	AAB48550	Aab48550 Ruminococ
29	112.5	5.0	954	5	AAO18656	Aao18656 R flavefa
30	112.5	5.0	954	8	ADI66758	Adi66758 R. flavef
31	111.5	5.0	622	8	ADG32266	Adg32266 Mutant B_
32	111.5	5.0	738	2	AAR13993	Aar13993 A.altocet
33	111	5.0	269	3	AAG18644	Aag18644 Arabidops
34	111	5.0	282	3	AAG18643	Aag18643 Arabidops
35	111	5.0	282	5	ABB93168	Abb93168 Herbicida
36	111	5.0	282	8	ADN72361	Adn72361 Thale cre
37	111	5.0	298	3	AAG18642	Aag18642 Arabidops
38	110.5	4.9	726	7	ADD22927	Add22927 Aspergill
39	108	4.8	282	3	AAG32464	Aag32464 Arabidops
40	108	4.8	282	5	ABB91456	Abb91456 Herbicida
41	107.5	4.8	545	2	AAW50908	Aaw50908 Cytophaga
42	107	4.8	280	3	AAB63197	Aab63197 Gene 21 h
43	107	4.8	540	8	ADN26066	Adn26066 Bacterial
44	106	4.7	365	4	ABU53216	Abu53216 Human met
45	106	4.7	457	6	ABU19526	Abu19526 Protein e

ALIGNMENTS

RESULT 1
AAY24914
ID AAY24914 standard; protein; 384 AA.
XX
AC AAY24914;
XX
DT 17-OCT-2003 (revised)
DT 25-AUG-1999 (first entry)
XX
DE Eisenia foetida coelomic cytolytic factor 1 protein.
XX
KW Eisenia foetida; coelomic cytolytic factor 1; CCF-1; cancer;
KW trypanosomal infection; bacterial infection; tumour therapy;
KW inflammation; immunology.
XX
OS Eisenia fetida.
XX
FH Key Location/Qualifiers
FT Peptide 1. .17
FT /label= signal
FT Protein 18. .384
FT /label= CCF-1
XX
PN WO9901220-A2.
XX
PD 24-JUN-1999.
XX
PF 16-DEC-1998; 98WO-EP008169.
XX
PR 17-DEC-1997; 97EP-00203974.
XX
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI De Baetselier P;
XX
DR WPI; 1999-385905/32.
DR N-PSDB; AAX83611.
XX
PT Eisenia foetida polypeptides derived from coelomic cytolytic factor 1.
XX
PS Claim 2; Page 48-49; 49pp; English.
XX
CC The present sequence represents the Eisenia foetida coelomic cytolytic
CC factor 1 (CCF-1). The protein has antiparasitic, antibacterial and
CC antiinflammatory activity. Recombinant coelomic cytolytic factor 1 (rCCF-
CC 1) is trypanolytic for the African trypanosome Trypanosoma brucei in a
CC dose-dependent manner. The trypanolytic activity of rCCF-1 can be
CC inhibited by anti-CCF-1 and anti-tumour necrosis factor (TNF)/TIP

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 17, 2005, 16:55:19 ; Search time 46.4282 Seconds
(without alignments)
795.793 Million cell updates/sec

Title: US-09-596-101C-3
Perfect score: 2240
Sequence: 1 MRWTLVVLCLLFGEGFAFTD.....DDEGDNNAMQVDYIRVYKRN 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	713	31.8	499	2	JC6141	beta 1,3-glucanase
2	369.5	16.5	877	2	JN0772	glucan endo-1,3-be
3	353	15.8	1324	2	T18265	endo-1,3(4)-beta-g
4	351.5	15.7	682	2	JQ0420	beta-1,3-glucanase
5	350	15.6	301	2	C87296	beta-glucanase [im
6	344.5	15.4	286	2	S48201	licheninase (EC 3.
7	314	14.0	467	2	JC6150	Gram-negative bact
8	312.5	14.0	411	2	JC7869	cell wall-lytic be
9	284	12.7	642	2	B72428	laminarinase - The
10	209	9.3	673	2	A49878	coagulation factor
11	179.5	8.0	466	2	T35164	probable secreted
12	176	7.9	465	2	AB2995	endo-1,3-1,4-beta-
13	176	7.9	482	2	H98288	endo-1,3-1,4-beta-
14	175.5	7.8	465	2	G95973	endo-1,3-1,4-beta-
15	167	7.5	465	2	H95369	EglC ENDO-1,3-1,4-
16	148	6.6	364	2	T17584	probable beta-1,3-
17	138.5	6.2	294	2	D70525	probable beta-1 -
18	132	5.9	419	2	T39920	probable glucanase
19	125.5	5.6	1144	2	A75132	hypothetical prote
20	125	5.6	857	2	B69798	hypothetical prote
21	116.5	5.2	878	2	A83748	endo-beta-N-acetyl
22	115	5.1	284	2	T06200	xyloglucan endo-1,
23	112.5	5.0	738	2	S14270	alcohol dehydrogen
24	112.5	5.0	954	1	S20907	endo-1,4-beta-xyla
25	111	5.0	282	2	A85354	hypothetical prote
26	110.5	4.9	856	2	T00349	Avicelase III - As
27	110	4.9	243	1	S15388	licheninase (EC 3.
28	109	4.9	781	2	A43866	neuraminidase - Vi
29	109	4.9	807	2	E82158	neuraminidase VC17
30	108	4.8	282	2	T02354	xyloglucan endo-1,
31	108	4.8	636	2	T37843	probable beta-gluc
32	108	4.8	720	2	S61143	KRE6 protein - yea
33	107.5	4.8	758	2	T48815	mixed-linked gluca
34	107.5	4.8	772	2	T02098	probable phosphati
35	106	4.7	238	1	S19012	licheninase (EC 3.
36	106	4.7	742	2	A49340	alcohol dehydrogen
37	106	4.7	782	1	G64157	probable organic s
38	105	4.7	802	2	A36910	xylanase, beta(1,3
39	104.5	4.7	239	1	A29091	licheninase (EC 3.
40	103.5	4.6	484	2	AH1419	beta-glucosidase h
41	103.5	4.6	484	2	AI1794	beta-glucosidase h
42	103.5	4.6	851	2	H84053	endo-beta-1,3-1,4
43	103	4.6	289	2	F71402	xyloglucan endo-1,
44	102.5	4.6	276	2	I40453	licheninase (EC 3.
45	102.5	4.6	334	1	S23498	licheninase (EC 3.

ALIGNMENTS

RESULT 1
JC6141
beta 1,3-glucanase (EC 3.2.1.-) precursor - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC6141; PC6037
R;Bachman, B.S.; McClay, D.R.
Proc. Natl. Acad. Sci. U.S.A. 93, 6808-6813, 1996
A;Title: Molecular cloning of the first metazoan beta-1,3 glucanase from eggs of the se
A;Reference number: JC6141; MUID:96270625; PMID:8692900
A;Accession: JC6141
A;Molecule type: mRNA
A;Residues: 1-499 <BAC>
A;Cross-references: UNIPROT:Q26660; GB:U49711; NID:g1488256; PIDN:AAC47235.1; PID:g1488
A;Accession: PC6037
A;Molecule type: protein
A;Residues: 21-40;197-209;329-344 <BA2>
A;Experimental source: egg
C;Comment: This enzyme functions in several extracellular activities including autocata
efense enzymes in plants.
C;Keywords: egg; glycosidase; hydrolase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-499/Product: beta 1,3-glucanase #status predicted <MAT>

Query Match 31.8%; Score 713; DB 2; Length 499;
Best Local Similarity 42.7%; Pred. No. 1.4e-49;
Matches 158; Conservative 48; Mismatches 88; Indels 76; Gaps 15;

```
Qy         26 IVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ 85
              :::|:||| |:   |:||:|| |||| ||: || : :||:|||||||||||||  | :
Db        179 LIFQEEFDSFNLDIWEHEMTAGGGGNWEFEYYTNNRSNSYVRDGKLFIKPTLTTDKL--- 235

Qy         86 TGAPFGTDFMYNGVLDVWAMYGA--CTNTDNNGCYRTGAAGD-IPPAMSARVRTFQKYSF 142
                    | : :| ||:|    |  ||     || |||:  : : |  |||:|| : :||
Db        236 -----GEGSLSSGTLDLWGSSPANLCTGNAWYGCSRTGSNDNLLNPIQSARLRTVESFSF 290

Qy        143 THGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGI 202
              :||: | ||:| |||||||||:||:   || || |||||:|: || | |:  |   |:
Db        291 KYGRLEVEAKLPTGDWLWPAIWLLPKHNGYGEWPASGEIDLVESRGNADIKDADGLSAGV 350

Qy        203 QKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALL 262
              :|||||||| |  | |     ||                :  :|:||||
Db        351 DQMGSTMHWGPFWPLNGY-----PK------------------THATKFYVDDE----- 381

Qy        263 DVPYPLIDANPWWVDFWEWGKPWLPQYEN-----DNPWAGGTN-LAPFDQNFHFILNVAV 316
                |:: :|   ||: |     ::||     |||||   | | |||| |: ||||||
Db        382 ----LLLNVDP-ATGFWDLG-----EFENDAPGIDNPWAYNPNKLTPFDQEFYLILNVAV 431

Qy        317 GGTNGFIPDGCINRGGD-----PALQKPWSNGDWYNDAMRKPFDARGNWKWTWDDEGDNN 371
              || | |          ||     ||  |||||       | : |:     |  ||:  |:
Db        432 GGVNYF---------GDGLTYTPA--KPWSNDS--PTASKDFWSDFNTWYPTWN--GEEA 476
```